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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/806,793

DATE: 08/05/2004

TIME: 09:00:11

Input Set : N:\Crif3\RULE60\10806793.raw

Output Set : N:\CRF4\08052004\J806793.raw

1 <110> APPLICANT: Johansen, Teit E.
2 Blom, Nikolaj
3 Hansen, Claus
4 <120> TITLE OF INVENTION: Novel Neurotrophic Factors
5 <130> FILE REFERENCE: 19313-001 DIV
6 <140> CURRENT APPLICATION NUMBER: US/10/806,793
7 <141> CURRENT FILING DATE: 2004-03-22
8 <150> PRIOR APPLICATION NUMBER: US/09/662,183
9 <151> PRIOR FILING DATE: 2000-09-14
10 <150> PRIOR APPLICATION NUMBER: DANISH 1998 00904
11 <151> PRIOR FILING DATE: 1998-07-06
12 <150> PRIOR APPLICATION NUMBER: USSN 60/092,229
13 <151> PRIOR FILING DATE: 1998-07-09
14 <150> PRIOR APPLICATION NUMBER: DANISH 1998 01048
15 <151> PRIOR FILING DATE: 1998-08-19
16 <150> PRIOR APPLICATION NUMBER: USSN 60/097,774
17 <151> PRIOR FILING DATE: 1998-08-25
18 <150> PRIOR APPLICATION NUMBER: DANISH 1998 01260
19 <151> PRIOR FILING DATE: 1998-10-05
20 <150> PRIOR APPLICATION NUMBER: USSN 60/103,908
21 <151> PRIOR FILING DATE: 1998-10-13
22 <150> PRIOR APPLICATION NUMBER: DANISH 1998 01265
23 <151> PRIOR FILING DATE: 1998-10-06
24 <150> PRIOR APPLICATION NUMBER: 09/347,613
25 <151> PRIOR FILING DATE: 2000-07-02
26 <160> NUMBER OF SEQ ID NOS: 43
27 <170> SOFTWARE: PatentIn Ver. 2.1
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31 <212> TYPE: DNA
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42 <220> FEATURE:
43 <221> NAME/KEY: sig_peptide
44 <222> LOCATION: (120)..(179)

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47 <222> LOCATION: (405)..(719)
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54 <222> LOCATION: (426)..(623)
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66 <222> LOCATION: (616)..(619)
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70      tccccaagcc cacctgggtg cctcttttct cctgaggct ccacttggtc tctccgcgc 119
71      atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167
72      Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
73      -95 -90 -85 -80
74      gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct gcc ccc cgc 215
75      Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
76      -75 -70 -65
77      gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac ctg ccg ggg 263
78      Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
79      -60 -55 -50
80      gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc 311
81      Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
82      -45 -40 -35
83      aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
84      Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
85      -30 -25 -20
86      tcc ccg cgg gtc cgc gcg gcg cgg ctg ggg ggc cgg gca gcg cgc tcg 407
87      Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
88      -15 -10 -5 -1 1
89      ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg 455
90      Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
91      5 10 15
92      cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc 503
93      Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg

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95 ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc 551
96 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
97          35          40          45
98 ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc 599
99 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
100          50          55          60          65
101 cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc 647
102 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
103          70          75          80
104 tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc 695
105 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
106          85          90          95
107 gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg ctccagggct ttgcagactg 749
108 Ala Thr Ala Cys Gly Cys Leu Gly
109          100          105
110 gacccttacc ggtggctctt cctgacctggg accctcccgc agagtcccac tagccagcgg 809
111 cctcagccag ggacgaaggc ctcaaagctg agaggccctt gccggtgggt gatgga 865
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115 <212> TYPE: PRT
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120 Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
121 -75 -70 -65
122 Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
123 -60 -55 -50
124 Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
125 -45 -40 -35
126 Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
127 -30 -25 -20
128 Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
129 -15 -10 -5 -1 1
130 Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
131 5 10 15
132 Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
133 20 25 30
134 Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
135 35 40 45
136 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
137 50 55 60 65
138 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
139 70 75 80
140 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
141 85 90 95
142 Ala Thr Ala Cys Gly Cys Leu Gly
143 100 105

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Input Set : N:\Crif3\RULE60\10806793.raw

Output Set: N:\CRF4\08052004\J806793.raw

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147 <212> TYPE: DNA
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151 <222> LOCATION: (7)..(717)
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153 <221> NAME/KEY: 5'UTR
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155 <220> FEATURE:
156 <221> NAME/KEY: 3'UTR
157 <222> LOCATION: (718)..(861)
158 <220> FEATURE:
159 <221> NAME/KEY: sig_peptide
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161 <220> FEATURE:
162 <221> NAME/KEY: mat_peptide
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168 <221> NAME/KEY: mat_peptide
169 <222> LOCATION: (379)..(717)
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171 <221> NAME/KEY: misc_structure
172 <222> LOCATION: (661)..(663)
173 <223> OTHER INFORMATION: CARBOHYD: glycosylated Asparagine as Asn122
174 <220> FEATURE:
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176 <222> LOCATION: (424)..(621)
177 <223> OTHER INFORMATION: DISULFID: Cys43-Cys108 disulfide bridge
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179 <221> NAME/KEY: misc_structure
180 <222> LOCATION: (505)..(705)
181 <223> OTHER INFORMATION: DISULFID: Cys70-Cys136 disulfide bridge
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183 <221> NAME/KEY: misc_structure
184 <222> LOCATION: (517)..(711)
185 <223> OTHER INFORMATION: DISULFID: Cys74-Cys138 disulfide bridge
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188 <222> LOCATION: (616)..(618)
189 <223> OTHER INFORMATION: DISULFID: Cys107-Cys107 interchain disulfide
190 bridge
191 <400> SEQUENCE: 3
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193 Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu

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Input Set : N:\Crf3\RULE60\10806793.raw

Output Set: N:\CRF4\08052004\J806793.raw

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194          -95          -90          -85
195 gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct 96
196 Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala
197          -80          -75          -70
198 cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct 144
199 Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala
200          -65          -60          -55
201 ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc 192
202 Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro
203          -50          -45          -40
204 cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc 240
205 Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro
206          -35          -30          -25          -20
207 gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga 288
208 Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg
209          -15          -10          -5
210 gcc cgg cgg ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct 336
211 Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro
212          -1 1          5          10
213 gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg 384
214 Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
215          15          20          25
216 ggc ccg ggc aac cgc gct cgg gca gcg ggg gcg ccg ggc tgc cgc ctg 432
217 Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
218          30          35          40          45
219 cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc 480
220 Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
221          50          55          60
222 gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg 528
223 Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
224          65          70          75
225 cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc 576
226 Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
227          80          85          90
228 ctg cga ccg ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga 624
229 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
230          95          100          105
231 ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg 672
232 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
233          110          115          120          125
234 aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc 717
235 Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
236          130          135          140
237 tgagggctcg ctccagggt ttgcagactg gacccttacc ggtggctett cctgcctggg 777
238 accctccgcg agagtccac tagccagcgg cctcagccag ggacgaagge ctcaaagctg 837
239 agaggccccct gccggtgggt gatg 861
241 <210> SEQ ID NO: 4
242 <211> LENGTH: 237
243 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 08/05/2004

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Input Set : N:\Crf3\RULE60\10806793.raw

Output Set: N:\CRF4\08052004\J806793.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 134,135

Seq#:6; Xaa Pos. 110,111

Seq#:7; Xaa Pos. 107,108

Seq#:27; N Pos. 1

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10806793.raw

Output Set: N:\CRF4\08052004\J806793.raw

L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:128
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:96
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:96
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0